

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: UNITED STATES OF AMERICA; DEPT. OF HEALTH AND HUMAN SERVICES

(ii) TITLE OF INVENTION: MOTILITY STIMULATING PROTEIN USEFUL IN CANCER DIAGNOSIS AND THERAPY

(iii) NUMBER OF SEQUENCES: 69

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: U.S.A.
(F) ZIP: 10154

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy Disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: 08/346,455
(B) FILING DATE: 28-NOV-1994

(viii) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: 08/249,182
(B) FILING DATE: 25-MAY-1994

(ix) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: 07/822,043
(B) FILING DATE: 17-JAN-1992

(viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 36,434
(C) DOCKET NUMBER: 2026-4149US3

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp His Val Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Leu Asp Val Tyr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Pro Ala Phe Lys
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Ala Glu Val Ser
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Glu Glu Val Thr Arg Pro Asn Tyr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr Asp Val Pro Trp Asn Glu Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly
1 5 10

Pro Thr Phe Lys
15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp
1 5 10

Asp Ile Thr Leu Val Pro Glu Thr Leu Gly Arg
15 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGGCAGCN ACRTGCCA

18

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGGCAYGTNG CTGCCAAC

18

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTGAAGGCA GGGTA

15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAYCCTGCNT TYAAG

15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTNACYTCY TCAGG

15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCTGARGARG TNACC

15

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

NGTNGCRTCR AATGGCACRT C

21

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAYGTGCCAT TYGAYGCNAC N

21

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTTDATRTTS TCRAATGGGG G

21

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCCCCATTG AGAACATCAA C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTNGTNGCN GTDATCCANA RGGGYTGGCC GCC

33

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCGGCCARC CCYTNTGGAT HACNGCNACN AAG

33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTTRAAGGTG GGGCCRTAGC CCACRAAGAC TGTYTGCAT

39

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCARACAG TCTTYGTGGG CTAYGGCCCC ACCTTYAAR

39

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gln Tyr Leu His Gln Tyr Gly Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Val Leu Asn Tyr Phe
1 5

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Tyr Leu Asn Ala Thr
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Tyr Pro Glu Ile Leu Thr Pro Ala Asp Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Xaa Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser
1 5 10
Ser Pro

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Thr Phe Pro Asn Leu Tyr Thr Phe Ala Thr Gly Leu
1 5 10
Tyr

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Asn Val Ile Ser Gly Pro Ile Asp Asp Tyr Asp
1 5 10
Tyr Asp Gly Leu His Asp Thr Glu Asp Lys
15 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE: Melanoma
- (H) CELL LINE: A2058
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Putative protein sequence of A2058 Autotaxin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Cys His Asp Phe Asp Glu Leu Cys Leu Lys Thr Ala
1 5 10
Arg Gly Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu
15 20
Val Arg Asn Glu Glu Asn Ala Cys His Cys Ser Glu
25 30 35
Asp Cys Leu Ala Arg Gly Asp Cys Cys Thr Asn Tyr
40 45
Gln Val Val Cys Lys Gly Glu Ser His Trp Val Asp
50 55 60
Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Pro
65 70
Ala Gly Phe Val Arg Pro Pro Leu Ile Ile Phe Ser
75 80
Val Asp Gly Phe Arg Ala Ser Tyr Met Lys Lys Gly
85 90 95
Ser Lys Val Met Pro Asn Ile Glu Lys Leu Arg Ser
100 105
Cys Gly Thr His Ser Pro Tyr Met Arg Pro Val Tyr
110 115 120
Pro Thr Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala
125 130
Thr Gly Leu Tyr Pro Glu Ser His Gly Ile Val Gly
135 140
Asn Ser Met Tyr Asp Pro Val Phe Asp Ala Thr Phe
145 150 155
His Leu Arg Gly Arg Glu Lys Phe Asn His Arg Trp
160 165
Trp Gly Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys
170 175 180
Gln Gly Val Lys Ala Gly Thr Phe Phe Trp Ser Val
185 190
Val Ile Pro His Glu Arg Arg Ile Leu Thr Ile Leu
195 200
Arg Trp Leu Thr Leu Pro Asp His Glu Arg Pro Ser
205 210 215
Val Tyr Ala Phe Tyr Ser Glu Gln Pro Asp Phe Ser
220 225
Gly His Lys Tyr Gly Pro Phe Gly Pro Glu Glu Ser
230 235 240
Ser Tyr Gly Ser Pro Phe Thr Pro Ala Lys Arg Pro
245 250
Lys Arg Lys Val Ala Pro Lys Arg Arg Gln Glu Arg
255 260
Pro Val Ala Pro Pro Lys Lys Arg Arg Arg Lys Ile
265 270 275
His Arg Met Asp His Tyr Ala Ala Glu Thr Arg Gln
280 285

Asp Lys Met Thr Asn Pro Leu Arg Glu Ile Asp Lys
290 295 300
Ile Val Gly Gln Leu Met Asp Gly Leu Lys Gln Leu
305 310
Lys Leu Arg Arg Cys Val Asn Val Ile Phe Val Gly
315 320
Asp His Gly Met Glu Asp Val Thr Cys Asp Arg Thr
325 330 335
Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp Asp
340 345
Ile Thr Leu Val Pro Gly Thr Leu Gly Arg Ile Arg
350 355 360
Ser Lys Phe Ser Asn Asn Ala Lys Tyr Asp Pro Lys
365 370
Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp
375 380
Gln His Phe Lys Pro Tyr Leu Lys Gln His Leu Pro
385 390 395
Lys Arg Leu His Tyr Ala Asn Asn Arg Arg Ile Glu
400 405
Asp Ile His Leu Leu Val Glu Arg Arg Trp His Val
410 415 420
Ala Arg Lys Pro Leu Asp Val Tyr Lys Lys Pro Ser
425 430
Gly Lys Cys Phe Phe Gln Gly Asp His Gly Phe Asp
435 440
Asn Lys Val Asn Ser Met Gln Thr Val Phe Val Gly
445 450 455
Tyr Gly Pro Thr Phe Lys Tyr Lys Thr Lys Val Pro
460 465
Pro Phe Glu Asn Ile Glu Leu Tyr Asn Val Met Cys
470 475 480
Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn Asn Gly
485 490
Thr His Gly Ser Leu Asn His Leu Leu Arg Thr Asn
495 500
Thr Phe Arg Pro Thr Met Pro Glu Glu Val Thr Arg
505 510 515
Pro Asn Tyr Pro Gly Ile Met Tyr Leu Gln Ser Asp
520 525
Asp Asp Leu Gly Cys Thr Cys Asp Asp Lys Val Glu
530 535 540
Pro Lys Asn Lys Leu Asp Glu Leu Asn Lys Arg Leu
545 550
His Thr Lys Gly Ser Thr Glu Glu Arg His Leu Leu
555 560
Tyr Gly Arg Pro Ala Val Leu Tyr Arg Thr Arg Tyr
565 570 575
Asp Ile Leu Tyr His Thr Asp Phe Glu Ser Gly Tyr
580 585
Ser Glu Ile Phe Leu Met Leu Leu Trp Thr Ser Tyr
590 595 600
Thr Val Ser Lys Gln Ala Glu Val Ser Ser Val Pro
605 610

Asp His Leu Thr Ser Cys Val Arg Pro Asp Val Arg
615 620
Val Ser Pro Ser Phe Ser Gln Asn Cys Leu Ala Tyr
625 630 635
Lys Asn Asp Lys Gln Met Ser Tyr Gly Phe Leu Phe
640 645
Pro Pro Tyr Leu Ser Ser Pro Glu Ala Lys Tyr
650 655 660
Asp Ala Phe Leu Val Thr Asn Met Val Pro Met Tyr
665 670
Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg
675 680
Val Leu Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly
685 690 695
Val Asn Val Ile Ser Gly Pro Ile Phe Asp Tyr Asp
700 705
Tyr Asp Gly Leu His Asp Thr Glu Asp Lys Ile Lys
710 715 720
Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr
725 730
His Tyr Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe
735 740
Thr Gln Pro Ala Asp Lys Cys Asp Gly Pro Leu Ser
745 750 755
Val Ser Ser Phe Ile Leu Pro His Arg Pro Asp Asn
760 765
Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys
770 775 780
Trp Val Glu Glu Leu Met Lys Met His Thr Ala Arg
785 790
Val Arg Asp Ile Glu His Leu Thr Ser Leu Asp Phe
795 800
Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu
805 810 815
Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu
820 825
Ile

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2946
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human
(B) STRAIN:

(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE: Melanoma
(H) CELL LINE: A2058
(I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Partial DNA Sequence
of A2058 Autotaxin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCTGCCATGA	CTTGATGAG	CTGTGTTGA	AGACAGCCG	40
TGGCTGGAG	TGTACTAAGG	ACAGATGTGG	AGAAGTCAGA	80
AATGAAGAAA	ATGCCTGTCA	CTGCTCAGAG	GACTGCTTGG	120
CCAGGGGAGA	CTGCTGTACC	AATTACCAAG	TGGTTTGCAA	160
AGGAGAGTCG	CATTGGGTTG	ATGATGACTG	TGAGGAAATA	200
AAGGCCGAG	AATGCCCTGC	AGGGTTTGT	CGCCCTCCAT	240
TAATCATCTT	CTCCGTGGAT	GGCTTCCGTG	CATCATACAT	280
GAAGAAAGGC	AGCAAAGTCA	TGCCTAATAT	TGAAAAACTA	320
AGGTCTTGTG	GCACACACTC	TCCCTACATG	AGGCCGGTGT	360
ACCCAACCAA	AACCTTCCT	AACTTATACA	CTTTGGCCAC	400
TGGGCTATAT	CCAGAACATC	ATGGAATTGT	TGGCAATTCA	440
ATGTATGATC	CTGTATTGTA	TGCCACTTT	CATCTGCGAG	480
GGCGAGAGAA	ATTAAATCAT	AGATGGTGGG	GAGGTCAACC	520
GCTATGGATT	ACAGCCACCA	AGCAAGGGT	GAAAGCTGGA	560
ACATTCTTT	GGTCTGTTGT	CATCCCTCAC	GAGCAGGAGAA	600
TATTAACCAT	ATTGCGGTGG	CTCACCCCTGC	CAGATCATGA	640
GAGGCCTTCG	GTCTATGCCT	TCTATTCTGA	GCAACCTGAT	680
TTCTCTGGAC	ACAAATATGG	CCCTTTCGGC	CCTGAGGAGA	720
GTAGTTATGG	CTCACCTTT	ACTCCGGCTA	AGAGACCTAA	760
GAGGAAAGTT	GCCCCTAAGA	GGAGACAGGA	AAGACCAGTT	800
GCTCCTCCAA	AGAAAAGAAG	AAGAAAAATA	CATAGGATGG	840
ATCATTATGC	TGCGGAAACT	CGTCAGGACA	AAATGACAAA	880
TCCTCTGAGG	GAAATCGACA	AAATTGTGGG	GCAATTAAATG	920
GATGGACTGA	AACAACCAA	ACTGCGTCGG	TGTGTCAACG	960
TCATCTTGT	CGGAGACCAT	GGAAATGGAAG	ATGTCACATG	1000
TGATAGAACT	GAGTTCTTGA	GTAATTACCT	AACTAATGTG	1040
GATGATATTA	CTTAGTGC	TGGAACTCTA	GGAAGAATTG	1080
GATCCAAATT	TAGCAACAAT	GCTAAATATG	ACCCCAAAGC	1120
CATTATTGCC	AATCTCACGT	GTAAAAAAC	AGATCAGCAC	1160
TTAAGCCTT	ACTTGAACAA	GCACCTTCCC	AAACGTTGAT	1200
ACTATGCCAA	CAACAGAAGA	ATTGAGGATA	TCCATTATT	1240
GGTGGAACGC	AGATGGCATG	TTGCAAGGAA	ACCTTTGGAT	1280
GTTTATAAGA	AACCATCAGG	AAAATGCTT	TTCCAGGGAG	1320
ACCACGGATT	TGATAACAAG	GTCAACAGCA	TGCAGACTGT	1360
TTTGTTAGGT	TATGGCCCAA	CATTTAAGTA	CAAGACTAAA	1400
GTGCCTCCAT	TTGAAAACAT	TGAACTTAC	AATGTTATGT	1440
GTGATCTCCT	GGGATTGAAG	CCAGCTCCTA	ATAATGGGAC	1480

CCATGGAAGT	TTGAATCATC	TCCTGCGCAC	TAATACCTTC	1520
AGGCCAACCA	TGCCAGAGGA	AGTTACCAGA	CCCAATTATC	1560
CAGGGATTAT	GTACCTTCAG	TCTGATTTCG	ACCTGGGCTG	1600
CACTTGTGAT	GATAAGGTAG	AGCCAAAGAA	CAAGTTGGAT	1640
GAACCTAACCA	AACGGCTTCA	TACAAAAGGG	TCTACAGAAG	1680
AGAGACACCT	CCTCTATGGG	CGACCTGCAG	TGCTTTATCG	1720
GACTAGATAT	GATATCTTAT	ATCACACTGA	CTTGAAAGT	1760
GGTTATAGTG	AAATATTCCCT	AATGCTACTC	TGGACATCAT	1800
ATACTGTTTC	CAAACAGGCT	GAGGTTCCA	GCGTTCCCTGA	1840
CCATCTGACC	AGTTGCGTCC	GGCCTGATGT	CCGTGTTCT	1880
CCGAGTTCA	GTCAGAACTG	TTTGGCCTAC	AAAAATGATA	1920
AGCAGATGTC	CTACGGATTG	CTCTTCCCTC	CTTATCTGAG	1960
CTCTTCACCA	GAGGCTAAAT	ATGATGCATT	CCTTGTAAACC	2000
AATATGGTTC	CAATGTATCC	TGCTTCAAA	CGGGTCTGGA	2040
ATTATTTCCA	AAGGGTATTG	GTGAAGAAAT	ATGCTTCGGA	2080
AAGAAATGGA	GTAAACGTGA	TAAGTGGACC	AATCTTCGAC	2120
TATGACTATG	ATGGCTTACA	TGACACAGAA	GACAAAATAA	2160
AACAGTACGT	GGAAGGCAGT	TCCATTCTG	TTCCAACCTCA	2200
CTACTACAGC	ATCATCACCA	GCTGTCTGGA	TTTCACTCAG	2240
CCTGCCGACA	AGTGTGACGG	CCCTCTCT	GTGTCTCCT	2280
TCATCCTGCC	TCACCGGCCT	GACAAAGAGG	AGAGCTGCAA	2320
TAGCTCAGAG	GACGAATCAA	AATGGGTAGA	AGAAACTCATG	2360
AAGATGCACA	CAGCTAGGGT	GCCTGACATT	GAACATCTCA	2400
CCAGCCTGGA	CTTCTTCGA	AAGACCAGCC	GCAGCTACCC	2440
AGAAATCCTG	ACACTCAAGA	CATACTGCA	TACATATGAG	2480
AGCGAGATTT	AACTTTCTGA	GCATCTGCAG	TACAGTCTTA	2520
TCAACTGGTT	GTATATTTTT	ATATTGTTT	TGTATTTATT	2560
AATTTGAAAC	CAGGACATTA	AAAATGTTAG	TATTTTAATC	2600
CTGTACCAAA	TCTGACATAT	TATGCCTGAA	TGACTCCACT	2640
GTTCCTCTCT	AATGCTTGAT	TTAGGTAGCC	TTGTGTTCTG	2680
AGTAGAGCTT	GTAATAAATA	CTGCAGCTTG	AGAAAAAGTG	2720
GAAGCTTCTA	AATGGTGCTG	CAGATTGAT	ATTTGCATTG	2760
AGGAAATATT	AATTTTCCAA	TGCACAGTTG	CCACATTAG	2800
TCCTGTACTG	TATGGAAACA	CTGATTTGT	AAAGTTGCCT	2840
TTATTTGCTG	TTAACTGTTA	ACTATGACAG	ATATATTTAA	2880
GCCTTATAAA	CCAATCTTAA	ACATAATAAA	TCACACATTC	2920
AGTTTAAAAA	AAAAAAAAAA	AAAAAAA	AAAAAA	2946

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE: teratocarcinoma
(H) CELL LINE: N-tera 2D1
(I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: N-tera 2D1 putative
ATX protein sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Cys Asp Asn Leu Cys Lys Ser Tyr Thr Ser Cys Cys
1 5 10
His Asp Phe Asp Glu Leu Cys Leu Lys Thr Ala Arg
15 20
Ala Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu Val
25 30 35
Arg Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp
40 45
Cys Leu Ala Arg Gly Asp Cys Cys Thr Asn Tyr Gln
50 55 60
Val Val Cys Lys Gly Glu Ser His Trp Val Asp Asp
65 70
Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Leu Gln
75 80
Val Asp Ser Pro Ser Ile Asn His Leu Leu Arg Gly
85 90 95
Trp Leu Pro Met Thr Ser Tyr Met Lys Lys Gly Ser
100 105
Lys Val Met Pro Asn Ile Glu Lys Leu Arg Ser Cys
110 115 120
Gly Thr His Ser Pro Tyr Met Arg Pro Val Tyr Pro
125 130
Thr Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr
135 140
Gly Leu Tyr Pro Glu Ser His Gly Ile Val Gly Asn
145 150 155
Ser Met Tyr Asp Pro Val Phe Asp Ala Thr Phe His
160 165
Leu Arg Gly Arg Glu Lys Phe Asn His Arg Trp Trp
170 175 180
Ala Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln
185 190
Arg Gly Glu Ser Trp Asn Ile Leu Leu Val Cys Cys
195 200
His Pro Ser Arg Ala Glu Ile Leu Thr Ile Leu Gln
205 210 215
Trp Leu Thr Leu Pro Asp His Glu Arg Pro Ser Val
220 225

Tyr Ala Phe Tyr Ser Glu Gln Pro Asp Phe Ser Gly
230 235 240
His Lys His Met Pro Phe Gly Pro Glu Met Pro Asn
245 250
Pro Leu Arg Glu Met His Lys Ile Val Gly Gln Leu
255 260
Met Asp Gly Leu Lys Gln Leu Lys Leu His Arg Cys
265 270 275
Val Asn Val Ile Phe Val Glu Thr Met Asp Gly Arg
280 285
Cys His Met Tyr Arg Thr Glu Phe Leu Ser Asn Tyr
290 295 300
Leu Thr Asn Val Asp Asp Ile Thr Leu Val Pro Gly
305 310
Thr Leu Gly Arg Ile Arg Ser Lys Phe Ser Asn Asn
315 320
Ala Lys Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu
325 330 335
Thr Cys Lys Lys Pro Asp Gln His Phe Lys Pro Tyr
340 345
Leu Lys Gln His Leu Pro Lys Arg Leu His Tyr Ala
350 355 360
Asn Asn Arg Arg Ile Glu Asp Ile His Leu Leu Val
365 370
Glu Arg Arg Trp His Val Ala Arg Lys Pro Leu Asp
375 380
Val Tyr Lys Lys Pro Ser Gly Asn Ala Phe Ser Arg
385 390 395
Glu Thr Thr Ala Phe Asp Asn Lys Val Asn Ser Met
400 405
Gln Thr Val Phe Val Gly Tyr Gly Pro Thr Phe Lys
410 415 420
Tyr Lys Thr Lys Val Pro Pro Phe Glu Asn Ile Glu
425 430
Leu Tyr Asn Val Met Cys Asp Leu Leu Gly Leu Lys
435 440
Pro Ala Pro Asn Asn Gly Thr His Phe Ser Leu Asn
445 450 455
His Leu Leu Arg Thr Asn Thr Phe Arg Pro Thr Met
460 465
Pro Glu Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile
470 475 480
Met Tyr Leu Gln Ser Asp Phe Asp Leu Gly Cys Thr
485 490
Cys Asp Asp Lys Val Glu Pro Lys Asn Lys Leu Asp
495 500
Glu Leu Asn Lys Arg Leu His Thr Lys Gly Ser Thr
505 510 515
Glu Glu Arg His Leu Leu Tyr Gly Asp Arg Pro Ala
520 525
Val Leu Tyr Arg Thr Arg Tyr Asp Ile Leu Tyr His
530 535 540
Thr Asp Phe Glu Ser Gly Tyr Ser Glu Ile Phe Leu
545 550

Met Pro Leu Trp Thr Ser Tyr Thr Val Ser Lys Gln
555 560
Ala Glu Val Ser Ser Val Pro Asp His Leu Thr Ser
565 570 575
Cys Val Arg Pro Asp Val Arg Val Ser Pro Ser Phe
580 585
Ser Gln Asn Cys Leu Ala Tyr Lys Asn Asp Lys Gln
590 595 600
Met Ser Tyr Gly Gly Leu Gly Pro Pro Tyr Leu Ser
605 610
Ser Ser Pro Glu Ala Lys Tyr Asp Ala Phe Leu Val
615 620
Thr Asn Met Val Pro Met Tyr Pro Ala Phe Lys Arg
625 630 635
Val Trp Asn Tyr Phe Gln Arg Val Leu Val Lys Lys
640 645
Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser
650 655 660
Gly Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His
665 670
Asp Thr Glu Asp Lys Ile Lys Gln Tyr Val Glu Gly
675 680
Ser Ser Ile Pro Val Pro Thr His Tyr Tyr Ser Ile
685 690 695
Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp
700 705
Lys Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile
710 715 720
Leu Pro His Arg Pro Asp Asn Glu Glu Ser Cys Asn
725 730
Ser Ser Glu Asp Glu Ser Lys Trp Val Glu Glu Leu
735 740
Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu
745 750 755
His Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser
760 765
Arg Ser Tyr Pro Glu Ile Leu Thr Leu Lys Thr Tyr
770 775 780
Leu His Thr Tyr Glu Ser Glu Ile
785

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2712
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

66

EI004875217US

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE: teratocarcinoma
(H) CELL LINE: N-tera 2D1
(I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: N-tera 2D1 ATX DNA sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGTGACAAC	TGTGTAAGAG	CTATACCA	GTG	TGCCATG	40
ACTTTGATGA	GCTGTGTTG	AAGACAGCCC	GTGCGTGGGA	80	
GTGTACTAAG	GACAGATGTG	GGGAAGTCAG	AAATGAAGAA	120	
AATGCCTGTC	ACTGCTCAGA	GGACTGCTTG	GCCAGGGGAG	160	
ACTGCTGAA	CAATTACCAA	GTGGTTGCA	AAGGAGAGTC	200	
GCATTGGGTT	GATGATGACT	GTGAGGAAAT	AAAGGCCGCA	240	
GAATGCCTGC	AGGTTTGTTC	GCCCTCCATT	AATCATCTTC	280	
TCCGTGGATG	GCTTCCGATG	ACATCATACA	TGAAGAAAGG	320	
CAGCAAAGTC	ATGCCTAATA	TTGAAAAACT	AAGGTCTTGT	360	
GGCACACACT	CTCCCTACAT	GAGGCCGGTG	TACCCAAC	400	
AAACCTTCC	TAACCTTAC	ACTTTGGCCA	CTGGGCTATA	440	
TCCAGAAATCA	CATGGAATTG	TTGGCAATT	AATGTATGAT	480	
CCTGTATTTG	ATGCCACTT	TCATCTGCGA	GGCGAGAGA	520	
AATTAAATCA	TAGATGGTGG	GGAGGTCAAC	CGCTATGGAT	560	
TACAGCCACC	AAGCAAAGGG	GTGAAAGCTG	GAACATTCTT	600	
TTGGTCTGTT	GTCATCCCTC	ACGAGCGGAG	ATATTAACCA	640	
TATTGCAGTG	GCTCACCTG	CCAGATCATG	AGAGGCCTTC	680	
GGTCTATGCC	TTCTATTCTG	AGCAACCTGA	TTTCTCTGGA	720	
CACAAACATA	TGCCTTCGG	CCCTGAGATG	ACAAATCCTC	760	
TGAGGGAAAT	GCACAAAATT	GTGGGGCAAT	TAATGGATGG	800	
ACTGAAACAA	CTAAAAC	CTGC	ATCGGTGTG	840	
TTTGTGAGA	CCATGGATGG	AAGATGTCAC	CAACGTCA	880	
CTGAGTTCTT	GAGTAATTAC	CTAACTAATG	ATGTATAGAA	920	
TACTTTAGTG	CCTGGAAC	TAGGAAGAAT	TGGATGATAT	960	
TTTAGCAACA	ATGCTAAATA	TCACCCCAA	TCGATCCAA	1000	
CCAATCTCAC	GTGTAAAAAA	CCAGATCAGC	1040		
TTACTTGAAA	CAGCACCTC	CCAAACGTT	1080		
AACAACAGAA	GAATTGAGGA	TATCCATT	1120		
GCAGATGGCA	TGTTGCAAGG	AAACCTTGG	1160		
GAAACCATCA	GGAAATGCTT	ATGTTTATAA	1200		
TTTGATAACA	AGGTCAACAG	TTTCCAGGGA	1240		
GTTATGGCCC	AACATTAAAG	GACCACGGCA	1280		
ATTGAAAAC	ATTGAACTT	GTGAGACTA	1320		
		GTGTGATCTC			

CTGGGATTGA	AGCCAGCTCC	TAATAATGGG	ACCCATGGAA	1360
GTTTGAATCA	TCTCCTGCAC	ACTAATAACCT	TCAGGCCAAC	1400
CATGCCAGAG	GAAGTTACCA	GACCCTATT	TCCAGGGATT	1440
ATGTACCTTC	AGTCTGATT	TGACCTGGC	TGCACCTGTG	1480
ATGATAAGGT	AGAGCCAAAG	AACAAGTTG	ATGAACTCAA	1520
CAAACGGCTT	CATACAAAAG	GGTCTACAGA	AGAGAGACAC	1560
CTCCTCTATG	GGGATCGACC	TGCAGTGCTT	TATCGGACTA	1600
GATATGATAT	CTTATATCAC	ACTGACTTTG	AAAGTGGTTA	1640
TAGTGAAATA	TTCCTAATGC	CACTCTGGAC	ATCATATACT	1680
GTTTCCAAAC	AGGCTGAGGT	TTCCAGCGTT	CCTGACCATC	1720
TGACCAGTTG	CGTCCGGCCT	GATGTCCGTG	TTTCTCCGAG	1760
TTTCAGTCAG	AACTGTTGG	CCTACAAAAA	TGATAAGCAG	1800
ATGTCCCTACG	GATTCCCTT	TCCTCCTTAT	CTGAGCTCTT	1840
CACCAGAGGC	TAAATATGAT	GCATTCCCTG	TAACCAATAT	1880
GGTTCCAATG	TATCCTGCTT	TCAAACGGGT	CTGGAATTAT	1920
TTCCAAAGGG	TATTGGTGAA	GAAATATGCT	TCGGAAAGAA	1960
ATGGAGTTAA	CGTGATAAGT	GGACCAATCT	TCGACTATGA	2000
CTATGATGGC	TTACATGACA	CAGAAGACAA	AATAAAACAG	2040
TACGTGGAAG	GCAGTTCCAT	TCCTGTTCCA	ACTCACTACT	2080
ACAGCATCAT	CACCAGCTGT	CTGGATTTC	CTCAGCCTGC	2120
CGACAAGTGT	GACGGCCCTC	TCTCTGTGTC	CTCCTTCATC	2160
CTGCCTCACC	GGCCTGACAA	CGAGGAGAGC	TGCAATAGCT	2200
CAGAGGACGA	ATCAAAATGG	GTAGAAGAAC	TCATGAAGAT	2240
GCACACAGCT	AGGGTGCCTG	ACATTGAACA	TCTCACCAGC	2280
CTGGACTTCT	TCCGAAAGAC	CAGCCGCAGC	TACCCAGAAAA	2320
TCCTGACACT	CAAGACATAC	CTGCATACAT	ATGAGAGCGA	2360
GATTTAACTT	TCTGAGCATC	TGCAGTACAG	TCTTATCAAC	2400
TGGTTGTATA	TTTTTATATT	GTTCAGTATTT	TTATTAATTT	2440
GAAACCAGGA	CATTAAAAAT	GTTCAGTATTT	TAATCCTGTA	2480
CCAAATCTGA	CATATTATGC	CTGAATGACT	CCACTGTTTT	2520
TCTCTAATGC	TTGATTTAGG	TAGCCTTGTG	TTCTGAGTAG	2560
AGCTTGTAAT	AAATACTGCA	GCTTGAGTTT	TTAGTGGAAAG	2600
CTTCTAAATG	GTGCTGCAGA	TTTGATATTT	GCATTGAGGA	2640
AATATTAATT	TTCCAATGCA	CAGTTGCCAC	ATTTAGTCCT	2680
GTACTGTATG	GAAACACTGA	TTTTGTAAAG	TT	2712

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:

(F) TISSUE TYPE: Liver
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: putative autotaxin protein sequence from human liver

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp
1 5 10
Ile Ser Leu Phe Thr Phe Ala Val Gly Val Asn Ile
15 20
Cys Leu Gly Phe Thr Ala His Arg Ile Lys Arg Ala
25 30 35
Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser
40 45
Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys
50 55 60
Gly Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro
65 70
Asp Cys Arg Cys Asp Asn Leu Cys Lys Ser Tyr Thr
75 80
Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys
85 90 95
Thr Ala Arg Ala Trp Glu Cys Thr Lys Asp Arg Cys
100 105
Gly Glu Val Arg Asn Glu Glu Asn Ala Cys His Cys
110 115 120
Ser Glu Asp Cys Leu Ala Arg Gly Asp Cys Cys Thr
125 130
Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp
135 140
Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu
145 150 155
Cys Leu Gln Val Cys Ser Pro Ser Ile Asn His Leu
160 165
Leu Arg Gly Trp Leu Pro Met Thr Ser Tyr Met Lys
170 175 180
Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu
185 190
Arg Ser Cys Gly Thr His Ser Pro Tyr Met Arg Pro
195 200
Val Tyr Pro Thr Lys Thr Phe Pro Asn Leu Tyr Thr
205 210 215
Leu Ala Thr Gly Leu Tyr Pro Glu Ser His Gly Ile
220 225
Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala
230 235 240

Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His
245 250
Arg Trp Trp Gly Gly Gln Pro Leu Trp Ile Thr Ala
255 260
Thr Lys Gln Arg Gly Glu Ser Trp Asn Ile Leu Leu
265 270 275
Val Cys Cys His Pro Ser Arg Ala Glu Ile Leu Thr
280 285
Ile Leu Gln Trp Leu Thr Leu Pro Asp His Glu Arg
290 295 300
Pro Ser Val Tyr Ala Phe Tyr Ser Glu Gln Pro Asp
305 310
Phe Ser Gly His Lys His Met Pro Phe Gly Pro Glu
315 320
Met Thr Asn Pro Leu Arg Glu Met His Lys Ile Val
325 330 335
Gly Gln Leu Met Asp Gly Leu Lys Gln Leu Lys Leu
340 345
His Arg Cys Val Asn Val Ile Phe Val Glu Thr Met
350 355 360
Asp Gly Arg Cys His Met Tyr Arg Thr Glu Phe Leu
365 370
Ser Asn Tyr Leu Thr Asn Val Asp Asp Ile Thr Leu
375 380
Val Pro Gly Thr Leu Gly Arg Ile Arg Ser Lys Phe
385 390 395
Ser Asn Asn Ala Lys Tyr Asp Pro Lys Ala Ile Ile
400 405
Ala Asn Leu Thr Cys Lys Lys Pro Asp Gln His Phe
410 415 420
Lys Pro Tyr Leu Lys Gln His Leu Pro Lys Arg Leu
425 430
His Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile His
435 440
Leu Leu Val Glu Arg Arg Trp His Val Ala Arg Lys
445 450 455
Pro Leu Asp Val Tyr Lys Lys Pro Ser Gly Asn Ala
460 465
Phe Ser Arg Glu Thr Thr Ala Phe Asp Asn Lys Val
470 475 480
Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly Pro
485 490
Thr Phe Lys Tyr Lys Thr Lys Val Pro Pro Phe Glu
495 500
Asn Ile Glu Leu Tyr Asn Val Met Cys Asp Leu Leu
505 510 515
Gly Leu Lys Pro Ala Pro Asn Asn Gly Thr His Gly
520 525
Ser Leu Asn His Leu Leu Arg Thr Asn Thr Phe Arg
530 535 540
Pro Thr Met Pro Glu Glu Val Thr Arg Pro Asn Tyr
545 550
Pro Gly Ile Met Tyr Leu Gln Ser Asp Phe Asp Leu
555 560

Gly Cys Thr Cys Asp Asp Lys Val Glu Pro Lys Asn
565 570 575
Lys Leu Asp Glu Leu Asn Lys Arg Leu His Thr Lys
580 585
Gly Ser Thr Glu Glu Arg His Leu Leu Tyr Gly Asp
590 595 600
Arg Pro Ala Val Leu Tyr Arg Thr Arg Tyr Asp Ile
605 610
Leu Tyr His Thr Asp Phe Glu Ser Gly Tyr Ser Glu
615 620
Ile Phe Leu Met Pro Leu Trp Thr Ser Tyr Thr Val
625 630 635
Ser Lys Gln Ala Glu Val Ser Ser Val Pro Asp His
640 645
Leu Thr Ser Cys Val Arg Pro Asp Val Arg Val Ser
650 655 660
Pro Ser Phe Ser Gln Asn Cys Leu Ala Tyr Lys Asn
665 670
Asp Lys Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro
675 680
Tyr Leu Ser Ser Ser Pro Glu Ala Lys Tyr Asp Ala
685 690 695
Phe Leu Val Thr Asn Met Val Pro Met Tyr Pro Ala
700 705
Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu
710 715 720
Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn
725 730
Val Ile Ser Gly Pro Ile Phe Asp Tyr Asp Tyr Asp
735 740
Gly Leu His Asp Thr Glu Asp Lys Ile Lys Gln Tyr
745 750 755
Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr
760 765
Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln
770 775 780
Pro Ala Asp Lys Cys Asp Gly Pro Leu Ser Val Ser
785 790
Ser Phe Ile Leu Pro His Arg Pro Asp Asn Glu Glu
795 800
Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val
805 810 815
Glu Glu Leu Met Lys Met His Thr Ala Arg Val Arg
820 825
Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg
830 835 840
Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu Thr Leu
845 850
Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile Xaa
855 860
Leu Ser Glu His Leu Gln Tyr Ser Leu Ile Asn Trp
865 870 875
Leu Tyr Ile Phe Ile Leu Phe Leu Tyr Leu Leu Ile
880 885

Xaa Asn Gln Asp Ile Lys Asn Val Ser Ile Leu Ile
890 895 900
Leu Tyr Gln Ile Xaa His Ile Met Pro Glu Xaa Leu
905 910
His Cys Phe Ser Leu Met Leu Asp Leu Gly Ser Leu
915 920
Val Phe Xaa Val Glu Leu Val Ile Asn Thr Ala Ala
925 930 935
Xaa Val Phe Ser Gly Ser Phe Xaa Met Val Leu Gln
940 945
Ile Xaa Tyr Leu His Xaa Gly Asn Ile Asn Phe Pro
950 955 960
Met His Ser Cys His Ile Xaa Ser Cys Thr Val Trp
965 970
Lys His Xaa Phe Cys Lys Val
975

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:
(A) DESCRIPTION: peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: ATX-204
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met His Thr Ala Arg Val Arg Asp
5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: ATX-205
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Ser Asn Asn Ala Lys Tyr Asp
5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: ATX-209
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Val Met Pro Asn Ile Glu Lys
5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: ATX-210
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Ala Arg Gly Trp Glu Cys Thr
5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-212
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Xaa Asp Ser Pro Trp Thr Xaa Ile Ser Gly Ser
5 10

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-214
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Leu Arg Ser Cys Gly Thr His Ser Pro Tyr Met
5 10

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-215/34A
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr Tyr Leu His Thr Tyr Glu Ser
5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp Gln
5 10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: ATX-216
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ile Val Gly Gln Leu Met Asp Gly
5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: ATX-218/44
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Thr Ser Arg Ser Tyr Pro Glu Ile Leu
5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9

- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No
(ix) FEATURE:
(A) NAME/KEY: ATX-223B/24
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Gln Ala Glu Val Ser Ser Val Pro Asp
5

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: ATX-224
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro Asp Asp Cys
5 10

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

(A) NAME/KEY: ATX-229

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu
5 10

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

(A) NAME/KEY: ATX-224/53

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu
1 5 10
Ser Ser Ser Pro
15

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE:

(A) DESCRIPTION: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE: Liver
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: 5' end of human liver ATX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGCAAGGA	GGAGCTCGTT	CCAGTCGTGT	CAAGATATAT	40
CCCTGTTCAC	TTTGCCGTT	GGAGTCAATA	TCTGCTTAGG	80
ATTCACTGCA	CATCGAATT	AGAGAGCAGA	AGGATGG	117

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE: Liver
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: N-terminal region
including transmembrane domain of liver
ATX protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp
1 5 10
Ile Ser Leu Phe Thr Phe Ala Val Gly Val Asn Ile
15 20
Cys Leu Gly Phe Thr Ala His Arg Ile Lys Arg Ala
25 30 35
Glu Gly Trp

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Yes

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Primer from 5' end of
4C11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCTCAGATAA GGAGGAAAGA G

21

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: Yes
(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Nested primers from 4C11
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GAATCCGTAG GACATCTGCT T

21

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: Yes
(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Nested primers from 4C11
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGTAGGCCAA ACAGTTCTGA C

21

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Nested sense primer deduced from ATX-101, wherein N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAYTCNATGC ARACNGTNTT YGTNG

25

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Nested primer of ATX-101, wherein N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTYGTNGGNT AYGGNCCNAC NTTYAA

26

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Nested primer deduced from ATX-103, wherein N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAYTAYCTNA CNAAYGTNGA YGAYAT

26

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Nested primer deduced from ATX-103, wherein N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAYGAYATNA CNCTNGTNCC NGGNAC

26

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Nested primer deduced from ATX-103, wherein N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TGYTTYGARY TNCARGARGC NGGNCCNCC

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCTGTCTTCA AACACAGC

18

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CTGGTGGCTG TAATCCATAG C

21

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Primer for 5' end of N-tera 2D1 sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CGTGAAGGCA AAGAGAACAC G

21

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3104
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
 - (A) NAME/KEY: N-tera 2D1 ATX cDNA
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AGTGCACTCC	GTGAAGGCAA	AGAGAACACG	CTGCAAAAGG	40
CTTTCCAATA	ATCCTCGACA	TGGCAAGGAG	GAGCTCGTTC	80
CAGTCGTGTC	AGATAATATC	CCTGTTCACT	TTTGCCGTTG	120
GAGTCAATAT	CTGCTTAGGA	TTCACTGCAC	ATCGAATTAA	160
GAGAGCAGAA	GGATGGGAGG	AAGGTCCCTC	TACAGTGCTA	200
TCAGACTCCC	CCTGGACCAA	CATCTCCGGA	TCTTGCAAGG	240
GCAGGTGCTT	TGAACTTCAA	GAGGCTGGAC	CTCCTGATTG	280
TCGCTGTGAC	AACTTGTGTA	AGAGCTATAC	CAGTTGCTGC	320
CATGACTTTG	ATGAGCTGTG	TTTGAAGACA	GCCCGTGCCT	360
GGGAGTGTAC	TAAGGACAGA	TGTGGAGAAG	TCAGAAATGA	400
AGAAAATGCC	TGTCACTGCT	CAGAGGACTG	CTTGGCCAGG	440
GGAGACTGCT	GTACCAATT	CCAAGTGGTT	TGCAAAGGAG	480
AGTCGCATTG	GGTTGATGAT	GACTGTGAGG	AAATAAAGGC	520
CGCAGAATGC	CCTGCAGGGT	TTGTTCGCCC	TCCATTAATC	560

ATCTTCTCCG	TGGATGGCTT	CCGTGCATCA	TACATGAAGA	600
AAGGCAGCAA	AGTCATGCCT	AATATTGAAA	AACTAAGGTC	640
TTGTGGCACA	CACTCGCCCC	ACATGAGGCC	GGTGTACCCA	680
ACTAAAACCT	TTCCTAACTT	ATACACTTG	GCCACTGGC	720
TATATCCAGA	ATCACATGGA	ATTGTTGCA	ATTCAATGTA	760
TGATCCTGTA	TTTGATGCCA	CTTTCATCT	GCGAGGGCGA	800
GAGAAATTG	ATCATAGATG	GTGGGGAGGT	CAACCGCTAT	840
GGATTACAGC	CACCAAGCAA	AGGGGTGAAA	GCTGGAACAT	880
TCTTTGGTC	TGTTGTCATC	CCTCACGAGC	GGAGATATTA	920
ACCATATTGC	AGTGGCTCAC	CCTGCCAGAT	CATGAGAGGC	960
TTCGGTCTAT	GCCTTCTATT	CTGAGCAACC	TGATTCTCT	1000
GGACACAAAT	ATGCCTTCG	GCCCTGAGAT	GACAAATCCT	1040
CTGAGGGAAA	TCGACAAAAT	TGTGGGCCAA	TTAATGGATG	1080
GAATGAAACA	ACTAAAACGT	CATCGGGTGTG	TCAACGTCAT	1120
CTTTGTCGGA	GACCATGGAA	TGGAAGATGT	CACATGTGAT	1160
AGAACTGAGT	TCTTGAGTAA	TTACCTAAT	AATGTGGATG	1200
ATATTACTTT	AGTGCCTGGG	ACTCTAGGAA	TTCGATCCAA	1240
ATTTAGCAAC	AATGCTAAAT	ATGACCCCAA	AGCCATTATT	1280
GCCAATCTCA	CGTGTAAAAA	ACCAGATCAG	CACTTTAAGC	1320
CTTACTTGAA	ACAGCACCTT	CCCAAACGTT	TGCACTATGC	1360
CAACAAACAGA	AGAATTGAGG	ATATCCATT	ATTGGTGGAA	1400
CGCAGATGGC	ATGTTGCAAG	GAAACCTTTG	GATGTTTATA	1440
AGAAACCATC	AGGAAAATGC	TTTTTCCAGG	GAGACCACGG	1480
ATTTGATAAC	AAGGTCAACA	GCATGCAGAC	TGTTTTGTA	1520
GGTTATGGCC	CAACATTAA	GTACAAGACT	AAAGTGCCTC	1560
CATTTGAAAAA	CATTGAACTT	TACAATGTTA	TGTGTGATCT	1600
CCTGGGATTG	AAGCCAGCTC	CTAATAATGG	GACCCATGGA	1640
AGTTTGAATC	ATCTCCTGCG	CACTAATACC	TTCAGGCCAA	1680
CCATGCCAGA	GGAAGTTACC	AGACCCAATT	ATCCAGGGAT	1720
TATGTACCTT	CAGTCTGATT	TTGACCTGGG	CTGCACTTGT	1760
GATGATAAGG	TAGAGCCAAA	GAACAAGTTG	GATGAACCTCA	1800
ACAAACGGCT	TCATACAAAAA	GGGTCTACAG	AAGAGAGACA	1840
CCTCCTCTAT	GGGCGACCTG	CAGTGCTTTA	TCGGACTAGA	1880
TATGATGTCT	TATATCACAC	TGACTTTGAA	AGTGGTTATA	1920
GTGAAATATT	CCTAATGCCA	CTCTGGACAT	CATAACTGT	1960
TTCCAAACAG	GCTGAGGTTT	CCAGCGTTCC	TGACCATCTG	2000
ACCAGTTGCG	TCCGGCTGTA	TGTCCGTGTT	TCTCCGAGTT	2040
TCAGTCAGAA	CTGTTGGCC	TACAAAAATG	ATAAGCAGAT	2080
GTCCTACGGA	TTCCCTTTTC	CTCCTTATCT	GAGCTTTCA	2120
CCAGAGGCTA	AATATGATGC	ATTCTTGTA	ACCAATATGG	2160
TTCCAATGTA	TCCTGTTTC	AAACGGGTCT	GGAATTATTT	2200
CCAAAGGGTA	TTGGTGAAGA	AATATGCTTC	GGAAAGAAAT	2240
GGAGTTAACG	TGATAAGTGG	ACCAATCTTC	GACTATGACT	2280
ATGATGGCTT	ACATGACACA	GAAGACAAAAA	AAAAACAGTA	2320
CGTGGAAAGC	AGTTCCATT	CTGTTCCAAC	TCACTACTAC	2360
AGCATCATCA	CCAGCTGTCT	GGATTTCACT	CAGCCTGCCG	2400
ACAAGTGTGA	CGGCCCTCTC	TCTGTGTCT	CCTTCATCCT	2440
CCGTCACCGG	CCTGACAACG	AGGAGAGCTG	CAATAGCTCA	2480
GAGGACGAAT	CAAAATGGGT	AGAAGAACTC	ATGAAGATGC	2520
ACACGGCTAG	GGTGCCTGAC	ATTGAACATC	TCACCAGCCT	2560
GGACTTCTTC	CGAAAGACCA	GCCGCAGCTA	CCCAGAAATC	2600
CTGACACTCA	AGACATACCT	GCATACATAT	GAGAGCGAGA	2640
TTTAACCTTC	TGAGCATCTG	CAGTACAGTC	TTATCAACTG	2680
GTTGTATATT	TTTATATTGT	TTTTGTATTT	ATTAATTGAA	2720

AACCAGGACA	TTAAAAATGT	TAGTATTTA	ATCCTGTACC	2760
AAATCTGACA	TATTATGCCT	GAATGACTCC	ACTGTTTTC	2800
TCTAATGCTT	GATTTAGGTA	GCCTTGTGTT	CTGAGTAGAG	2840
CTTGTAAATAA	ATACTGCAGC	TTGAGTTTT	AGTGGAAAGCT	2880
TCTAAATGGT	GCTGCAGATT	TGATATTGTC	ATTGAGGAAA	2920
TATTAATTTC	CCAATGCACA	GTTGCCACAT	TTAGTCCTGT	2960
ACTGTATGGA	AACACTGATT	TTGTAAAGTT	GCCTTTATTT	3000
GCTGTTAACT	GTAACTATG	ACAGATATAT	TTAAGCCTTA	3040
TAAACCAATC	TTAACACATAA	TAAATCACAC	ATTCAAGTTTT	3080
TTCTGGTAAA	AAAAAAAAAA	AAAA		3104

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
 - (A) NAME/KEY: N-tera 2D1 ATX protein
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met	Ala	Arg	Arg	Ser	Ser	Phe	Gln	Ser	Cys	Gln	Ile	Ile	Ser	Leu	Phe
1				5				10					15		
Thr	Phe	Ala	Val	Gly	Val	Asn	Ile	Cys	Leu	Gly	Phe	Thr	Ala	His	Arg
	20				25								30		
Ile	Lys	Arg	Ala	Glu	Gly	Trp	Glu	Glu	Gly	Pro	Pro	Thr	Val	Leu	Ser
	35					40						45			
Asp	Ser	Pro	Trp	Thr	Asn	Ile	Ser	Gly	Ser	Cys	Lys	Gly	Arg	Cys	Phe
	50				55						60				
Glu	Leu	Gln	Glu	Ala	Gly	Pro	Pro	Asp	Cys	Arg	Cys	Asp	Asn	Leu	Cys
	65					70			75				80		
Lys	Ser	Tyr	Thr	Ser	Cys	Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys
					85				90				95		
Thr	Ala	Arg	Ala	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	Val	Arg
					100			105				110			
Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly
					115			120				125			
Asp	Cys	Cys	Thr	Asn	Tyr	Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp
					130			135			140				
Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	Ala	Gly
	145				150				155				160		

Phe Val Arg Pro Pro Leu Ile Ile Phe Ser Val Asp Gly Phe Arg Ala
165 170 175
Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu
180 185 190
Arg Ser Cys Gly Thr His Ser Pro His Met Arg Pro Val Tyr Pro Thr
195 200 205
Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr Gly Leu Tyr Pro Glu
210 215 220
Ser His Gly Ile Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala
225 230 235 240
Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His Arg Trp Trp Gly
245 250 255
Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln Arg Gly Glu Ser Trp
260 265 270
Asn Ile Leu Leu Val Cys Cys His Pro Ser Arg Ala Glu Ile Leu Thr
275 280 285
Ile Leu Gln Trp Leu Thr Leu Pro Asp His Glu Arg Leu Arg Ser Met
290 295 300
Pro Ser Ile Leu Ser Asn Leu Ile Ser Leu Asp Thr Asn Met Pro Phe
305 310 315 320
Gly Pro Glu Met Thr Asn Pro Leu Arg Glu Ile Asp Lys Ile Val Gly
325 330 335
Gln Leu Met Asp Gly Leu Lys Gln Leu Lys Leu His Arg Cys Val Asn
340 345 350
Val Ile Phe Val Gly Asp His Gly Met Glu Asp Val Thr Cys Asp Arg
355 360 365
Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp Asp Ile Thr Leu
370 375 380
Val Pro Gly Thr Leu Gly Ile Arg Ser Lys Phe Ser Asn Asn Ala Lys
385 390 395 400
Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp
405 410 415
Gln His Phe Lys Pro Tyr Leu Lys Gln His Leu Pro Lys Arg Leu His
420 425 430
Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile His Leu Leu Val Glu Arg
435 440 445
Arg Trp His Val Ala Arg Lys Pro Leu Asp Val Tyr Lys Lys Pro Ser
450 455 460
Gly Lys Cys Phe Phe Gln Gly Asp His Gly Phe Asp Asn Lys Val Asn
465 470 475 480
Ser Met Gln Thr Val Phe Val Gly Tyr Gly Pro Thr Phe Lys Tyr Lys
485 490 495
Thr Lys Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr Asn Val Met Cys
500 505 510
Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn Asn Gly Thr His Gly Ser
515 520 525
Leu Asn His Leu Leu Arg Thr Asn Thr Phe Arg Pro Thr Met Pro Glu
530 535 540
Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile Met Tyr Leu Gln Ser Asp
445 450 455 460
Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys Val Glu Pro Lys Asn Lys
565 570 575
Leu Asp Glu Leu Asn Lys Arg Leu His Thr Lys Gly Ser Thr Glu Glu
580 585 590

Arg His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr Arg Thr Arg Tyr
595 600 605
Asp Val Leu Tyr His Thr Asp Phe Glu Ser Gly Tyr Ser Glu Ile Phe
610 615 620
Leu Met Pro Leu Trp Thr Ser Tyr Thr Val Ser Lys Gln Ala Glu Val
625 630 635 640
Ser Ser Val Pro Asp His Leu Thr Ser Cys Val Arg Pro Asp Val Arg
645 650 655
Val Ser Pro Ser Phe Ser Gln Asn Cys Leu Ala Tyr Lys Asn Asp Lys
660 665 670
Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro
675 680 685
Glu Ala Lys Tyr Asp Ala Phe Leu Val Thr Asn Met Val Pro Met Tyr
690 695 700
Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu Val Lys
705 710 715 720
Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly Pro Ile
725 730 735
Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys Ile Lys
740 745 750
Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr Tyr Ser
755 760 765
Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys Cys Asp
770 775 780
Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Arg His Arg Pro Asp Asn
785 790 795 800
Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val Glu Glu
805 810 815
Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His Leu Thr
820 825 830
Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu
835 840 845
Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile
850 855 860

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3251
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(ix) FEATURE:

(A) NAME/KEY: A2058 ATX cDNA
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CGTGAAGGCA	AAGAGAACAC	GCTGCAAAAG	GCTTCCAAGA	40
ATCCTCGACA	TGGCAAGGAG	GAGCTCGTTC	CAGTCGTGTC	80
AGATAATATC	CCTGTTCACT	TTTGCCGTTG	GAGTCAGTAT	120
CTGCTTAGGA	TTCACTGCAC	ATCGAATTAA	GAGAGCAGAA	160
GGATGGGAGG	AAGGTCTCC	TACAGTGCTA	TCAGACTCCC	200
CCTGGACCAA	CATCTCCGGA	TCTTGCAAGG	GCAGGTGCTT	240
TGAACCTCAA	GAGGCTGGAC	CTCCTGATTG	TCGCTGTGAC	280
AACTTGTGTA	AGAGCTATAAC	CAGTTGCTGC	CATGACTTTG	320
ATGAGCTGTG	TTTGAAGACA	GCCCCGTGGCT	GGGAGTGTAC	360
TAAGGACAGA	TGTGGAGAAG	TCAGAAATGA	AGAAAATGCC	400
TGTCACTGCT	CAGAGGACTG	CTTGGCCAGG	GGAGACTGCT	440
GTACCAATTAA	CCAAGTGGTT	TGCAAAGGAG	AGTCGCATTG	480
GGTTGATGAT	GAATGTGAGG	AAATAAAGGC	CGCAGAAATGC	520
CCTGCAGGGT	TTGTTCGCCC	TCCATTAAATC	ATCTTCTCCG	560
TGGATGGCTT	CCGTGCATCA	TACATGAAGA	AAGGCAGCAA	600
AGTCATGCCT	AATATTGAAA	AACTAAGTC	TTGTGGCACA	640
CACTCTCCCT	ACATGAGGCC	GGTGTACCCA	ACTAAAACCT	680
TTCCTTAACCT	ATACACTTTG	GCCACTGGC	TATATCCAGA	720
ATCACATGGA	ATTGTTGGCA	ATTCAATGTA	TGATCCTGTA	760
TTTGATGCCA	CTTTCATCT	GCGAGGGCGA	GAGAAATTAA	800
ATCATAGATG	GTGGGGAGGT	CAACCGCTAT	GGATTACAGC	840
CACCAAGCAA	GGGGTGAAAG	CTGGAACATT	CTTTGGTCT	880
GTTGTATCC	CTCACGAGCG	GAGAATATTA	ACCATATTGC	920
GGTGGCTCAC	CCTGCCAGAT	CATGAGAGGC	CTTCGGTCTA	960
TGCCTTCTAT	TCTGAGCAAC	CTGATTTCTC	TGGACACAAA	1000
TATGGCCCTT	TCGGCCCTGA	GGAGAGTAGT	TATGGCTCAC	1040
CTTTTACTCC	GGCTAAGAGA	CCTAAGAGGA	AAGTTGCC	1080
TAAGAGGAGA	CAGGAAAGAC	CAGTTGCTCC	TCCAAAGAAA	1120
AGAAGAAAGAA	AAATACATAG	GATGGATCAT	TATGCTGCGG	1160
AAACTCGTCA	GGACAAAATG	ACAAATCCTC	TGAGGGAAAT	1200
CGACAAAATT	GTGGGGCAAT	TAATGGATGG	ACTGAAACAA	1240
CTAAAACCTGC	GTCGGTGTGT	CAACGTCATC	TTTGTGGAG	1280
ACCATGGAAT	GGAAGATGTC	ACATGTGATA	GAACTGAGTT	1320
CTTGAGTAAT	TACCTAACTA	ATGTGGATGA	TATTACTTTA	1360
GTGCCTGGAA	CTCTAGGAAG	AATTGATCC	AAATTAGCA	1400
ACAATGCTAA	ATATGACCCC	AAAGCCATTA	TTGCCAATCT	1440
CACGTGTAAA	AAACCAGATC	AGCACTTAA	GCCTTACTTG	1480
AAACAGGCCACC	TTCCCAAACG	TTTGCACTAT	GCCAACAAACA	1520
GAAGAATTGA	GGATATCCAT	TTATTGGTGG	AACGCAGATG	1560
GCATGTTGCA	AGGAAACCTT	TGGATGTTA	TAAGAAACCA	1600
TCAGGAAAAT	GCTTTTCCA	GGGAGACAC	GGATTTGATA	1640
ACAAGGTCAA	CAGCATGCAG	ACTGTTTTG	TAGGTTATGG	1680
CCCAACATTT	AAGTACAAGA	CTAAAGTGCC	TCCATTGAA	1720
AACATTGAAC	TTTACAATGT	TATGTGTGAT	CTCCTGGGAT	1760
TGAAGCCAGC	TCCTAATAAT	GGGACCCATG	GAAGTTGAA	1800
TCATCTCCTG	CGCACTAATA	CCTTCAGGCC	AACCATGCCA	1840
GAGGAAGTTA	CCAGACCAA	TTATCCAGGG	ATTATGTACC	1880
TTCAGTCTGA	TTTTGACCTG	GGCTGCACTT	GTGATGATAA	1920
GGTAGAGCCA	AAGAACAAAGT	TGGATGAACT	CAACAAACGG	1960
CTTCATACAA	AAGGGTCTAC	AGAAGAGAGA	CACCTCCTCT	2000

ATGGGCGACC	TGCAGTGCTT	TATCGGACTA	GATATGATAT	2040
CTTATATCAC	ACTGACTTTG	AAAGTGGTTA	TAGTGAAATA	2080
TTCCTAATGC	TACTCTGGAC	ATCATATACT	GTTCACAAAC	2120
AGGCTGAGGT	TTCCAGCGTT	CCTGACCATC	TGACCAGTTG	2160
CGTCCGGCCT	GATGTCCGTG	TTTCTCCGAG	TTTCAGTCAG	2200
AACTGTTGG	CCTACAAAAA	TGATAAGCAG	ATGTCCCTACG	2240
GATTCCCTCTT	TCCTCCTTAT	CTGAGCTCTT	CACCAAGGGC	2280
TAAATATGAT	GCATTCCTTG	TAACCAATAT	GGTTCCAATG	2320
TATCCTGCTT	TCAAACGGGT	CTGGAATTAT	TTCCAAAGGG	2360
TATTGGTGAA	GAAATATGCT	TCGGAAAGAA	ATGGAGTTAA	2400
CGTGATAAGT	GGACCAATCT	TCGACTATGA	CTATGATGGC	2440
TTACATGACA	CAGAAGACAA	AATAAAACAG	TACGTGGAAG	2480
GCAGTTCCAT	TCCTGTTCCA	ACTCACTACT	ACAGCATCAT	2520
CACCAGCTGT	CTGGATTTC	CTCAGCCTGC	CGACAAGTGT	2560
GACGGCCCTC	TCTCTGTGTC	CTCCTTCATC	CTGCCTCACC	2600
GGCCTGACAA	CGAGGAGAGC	TGCAATAGCT	CAGAGGACGA	2640
ATCAAAATGG	GTAGAAGAAC	TCATGAAGAT	GCACACAGCT	2680
AGGGTGCCTG	ACATTGAACA	TCTCACCAGC	CTGGACTTCT	2720
TCCGAAAGAC	CAGCCGCAGC	TACCCAGAAA	TCCTGACACT	2760
CAAGACATAC	CTGCATACAT	ATGAGAGCGA	GATTTAACTT	2800
TCTGAGGCATC	TGCAGTACAG	TCTTATCAAC	TGGTTGTATA	2840
TTTTTATATT	GTTTTTGTAT	TTATTAAATT	GAAACCAGGA	2880
CATTAAAAAT	GTTAGTATT	TAATCCTGTA	CCAAATCTGA	2920
CATATTATGC	CTGAATGACT	CCACTGTTT	TCTCTAATGC	2960
TTGATTAGG	TAGCCTGTG	TTCTGAGTAG	AGCTTGTAA	3000
AAATACTGCA	GCTTGAGAAA	AAAGTGGAAAGC	TTCTAAATGG	3040
TGCTGCAGAT	TTGATATTG	CATTGAGGAA	ATATTAATT	3080
TCCAATGCAC	AGTTGCCACA	TTTAGTCCTG	TACTGTATGG	3120
AAACACTGAT	TTTGAAAGT	TGCCTTTATT	TGCTGTTAAC	3160
TGTTAACTAT	GACAGATATA	TTAAGCCTT	ATAAACCAAT	3200
CTTAAACATA	ATAAATCACA	CATTAGTTT	AAAAAAAAAA	3240
AAAAAAAAAA	A			3251

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: A2058 ATX protein
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Ile
1 5 10
Ile Ser Leu Phe Thr Phe Ala Val Gly Val Ser Ile
15 20
Cys Leu Gly Phe Thr Ala His Arg Ile Lys Arg Ala
25 30 35
Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser
40 45
Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys
50 55 60
Gly Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro
65 70
Asp Cys Arg Cys Asp Asn Leu Cys Lys Ser Tyr Thr
75 80
Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys
85 90 95
Thr Ala Arg Gly Trp Glu Cys Thr Lys Asp Arg Cys
100 105
Gly Glu Val Arg Asn Glu Glu Asn Ala Cys His Cys
110 115 120
Ser Glu Asp Cys Leu Ala Arg Gly Asp Cys Cys Thr
125 130
Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp
135 140
Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu
145 150 155
Cys Pro Ala Gly Phe Val Arg Pro Pro Leu Ile Ile
160 165
Phe Ser Val Asp Gly Phe Arg Ala Ser Tyr Met Lys
170 175 180
Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu
185 190
Arg Ser Cys Gly Thr His Ser Pro Tyr Met Arg Pro
195 200
Val Tyr Pro Thr Lys Thr Phe Pro Asn Leu Tyr Thr
205 210 215
Leu Ala Thr Gly Leu Tyr Pro Glu Ser His Gly Ile
220 225
Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala
230 235 240
Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His
245 250
Arg Trp Trp Gly Gly Gln Pro Leu Trp Ile Thr Ala
255 260
Thr Lys Gln Gly Val Lys Ala Gly Thr Phe Phe Trp
265 270 275
Ser Val Val Ile Pro His Glu Arg Arg Ile Leu Thr
280 285
Ile Leu Arg Trp Leu Thr Leu Pro Asp His Glu Arg
290 295 300
Pro Ser Val Tyr Ala Phe Tyr Ser Glu Gln Pro Asp
305 310

Phe Ser Gly His Lys Tyr Gly Pro Phe Gly Pro Glu
315 320
Glu Ser Ser Tyr Gly Ser Pro Phe Thr Pro Ala Lys
325 330 335
Arg Pro Lys Arg Lys Val Ala Pro Lys Arg Arg Gln
340 345
Glu Arg Pro Val Ala Pro Pro Lys Lys Arg Arg Arg
350 355 360
Lys Ile His Arg Met Asp His Tyr Ala Ala Glu Thr
365 370
Arg Gln Asp Lys Met Thr Asn Pro Leu Arg Glu Ile
375 380
Asp Lys Ile Val Gly Gln Leu Met Asp Gly Leu Lys
385 390 395
Gln Leu Lys Leu Arg Arg Cys Val Asn Val Ile Phe
400 405
Val Gly Asp His Gly Met Glu Asp Val Thr Cys Asp
410 415 420
Arg Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val
425 430
Asp Asp Ile Thr Leu Val Pro Gly Thr Leu Gly Arg
435 440
Ile Arg Ser Lys Phe Ser Asn Asn Ala Lys Tyr Asp
445 450 455
Pro Lys Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys
460 465
Pro Asp Gln His Phe Lys Pro Tyr Leu Lys Gln His
470 475 480
Leu Pro Lys Arg Leu His Tyr Ala Asn Asn Arg Arg
485 490
Ile Glu Asp Ile His Leu Leu Val Glu Arg Arg Trp
495 500
His Val Ala Arg Lys Pro Leu Asp Val Tyr Lys Lys
505 510 515
Pro Ser Gly Lys Cys Phe Phe Gln Gly Asp His Gly
520 525
Phe Asp Asn Lys Val Asn Ser Met Gln Thr Val Phe
530 535 540
Val Gly Tyr Gly Pro Thr Phe Lys Tyr Lys Thr Lys
545 550
Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr Asn Val
555 560
Met Cys Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn
565 570 575
Asn Gly Thr His Gly Ser Leu Asn His Leu Leu Arg
580 585
Thr Asn Thr Phe Arg Pro Thr Met Pro Glu Glu Val
590 595 600
Thr Arg Pro Asn Tyr Pro Gly Ile Met Tyr Leu Gln
605 610
Ser Asp Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys
615 620
Val Glu Pro Lys Asn Lys Leu Asp Glu Leu Asn Lys
625 630 635

Arg Leu His Thr Lys Gly Ser Thr Glu Glu Arg His
640 645
Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr Arg Thr
650 655 660
Arg Tyr Asp Ile Leu Tyr His Thr Asp Phe Glu Ser
665 670
Gly Tyr Ser Glu Ile Phe Leu Met Leu Leu Trp Thr
675 680
Ser Tyr Thr Val Ser Lys Gln Ala Glu Val Ser Ser
685 690 695
Val Pro Asp His Leu Thr Ser Cys Val Arg Pro Asp
700 705
Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys Leu
710 715 720
Ala Tyr Lys Asn Asp Lys Gln Met Ser Tyr Gly Phe
725 730
Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro Glu Ala
735 740
Lys Tyr Asp Ala Phe Leu Val Thr Asn Met Val Pro
745 750 755
Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe
760 765
Gln Arg Val Leu Val Lys Lys Tyr Ala Ser Glu Arg
770 775 780
Asn Gly Val Asn Val Ile Ser Gly Pro Ile Phe Asp
785 790
Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys
795 800
Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro Val
805 810 815
Pro Thr His Tyr Tyr Ser Ile Ile Thr Ser Cys Leu
820 825
Asp Phe Thr Gln Pro Ala Asp Lys Cys Asp Gly Pro
830 835 840
Leu Ser Val Ser Ser Phe Ile Leu Pro His Arg Pro
845 850
Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu
855 860
Ser Lys Trp Val Glu Glu Leu Met Lys Met His Thr
865 870 875
Ala Arg Val Arg Asp Ile Glu His Leu Thr Ser Leu
880 885
Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu
890 895 900
Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr
905 910
Glu Ser Glu Ile
916